SEQUENCE LISTING

<110> MACK, DAVID
GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST CANCER MODULATORS

<130> A-67860-3/DJB/JJD

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<141> 2000-03-15

<150> US 09/268,865
<151> 1999-03-15

<150> US 09/450,810
<151> 1999-11-29

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<151> 1999-12-02

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<170> PatentIn Ver. 2.1

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35 40 45

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50 55 60

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Asp Tyr Thr Ala Thr Ile Tyr Leu Arg Gln Arg Trp Met Asp Gln Arg
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Glu Phe Leu Trp Val Pro Asp Thr Tyr Ile Val Glu Ser Lys Lys Ser
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Asn Ile Ile Asn Ser Ser Ile Ser Ser Phe Lys Arg Lys Ile Ser Phe
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Arg Ile Val Asp Tyr Phe Thr Ile Gln Asn Pro Ser Asn Val Asp His
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<212> PRT
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    50                  55                  60

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Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
                85                  90                  95

Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
            100                 105                 110

Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
        115                 120                 125

Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
    130                 135                 140

Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
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Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
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Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
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Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro
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Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met
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Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
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Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys
        275                 280                 285

Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu
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Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn
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Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg
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Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn
                405                 410                 415

Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg
            420                 425                 430

Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu
        435                 440                 445

Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Asp
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<211> 1958

<212> DNA
<213> Homo sapiens

<400> 11
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attattttgt aagttgtgga aaaagctaat tgtagttttc attatgaagt tttcccaata 1920
aaccaggtat tctaaacttg aaaaaaaaaa aaaaaaaa 1958

<210> 12
<211> 582
<212> DNA
<213> Homo sapiens

<400> 12
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cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcatcat cctggtgatc tgtttcatcc tctccttctt cgccctctgt 300
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gccaaccctg ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga ttggctgtgc cttcttcttc tgctgcctcc ccaactacga agatgacctt 540
ctgggcaatg ccaagcccag gtacttctac acatctgcct aa 582

<210> 13
<211> 193
<212> PRT

<213> Homo sapiens

<400> 13
Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
20 25 30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45

Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
100 105 110

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
115 120 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
130 135 140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175

Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190

Ala

<210> 14
<211> 193
<212> PRT
<213> Mouse

<400> 14
Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
20 25 30

Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
35 40 45

Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
50 55 60

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Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
 65                  70                  75                  80

Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
                85                  90                  95

Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
            100                 105                 110

Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
        115                 120                 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
    130                 135                 140

Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145                 150                 155                 160

Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
                165                 170                 175

Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
            180                 185                 190

Ala
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<210> 15
<211> 124
<212> PRT
<213> Rat

<400> 15

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Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr Leu Phe Cys Gly Phe
  1               5                  10                  15

Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly
            20                  25                  30

Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
        35                  40                  45

Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
    50                  55                  60

Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
 65                  70                  75                  80

Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
                85                  90                  95

Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu
            100                 105                 110

Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
        115                 120
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<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 16
Cys Ser Tyr Ser Ala Pro Ser Pro Ser Thr Ser Ser Arg Trp Pro
1 5 10 15

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 17
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro
1 5 10 15

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
Cys Gly Gly Asn Ala Pro Lys Arg Gly Gly Gly Arg Gly Ser Tyr
1 5 10 15

<210> 19
<211> 1970
<212> DNA
<213> Mouse

<400> 19
gtcaccggaa tcaaggtgtg gctggagcgc cgctcccccg ccgycagccc gkkggccgcg 60
tcttcggggg agccgcctct tccttwattc ggckcygaca gcgctcgcag gaccactctt 120
ggccgctgct cctgcccggc gttcctccgc tccgcgcccg ccgccaccga cgacatgctg 180
cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc ccctgctgct gctcagcgcc 240
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cagacatcgt cgctttggtg gaggtgtttc gacgagggcg gcggcagcgg ctcctacgac 360
gatggctgcc agagcctcat ggagtacgca tggggacgag cagctgcagc cacgcttttc 420
tgtggcttta tcatcctgtg catctgcttc attctctcgt tcttcgccct gtgtggaccc 480
cagatgcttg ttttcctgag agtcattgga ggcctcctcg cactggctgc catattccag 540
atcatctccc tggtaatcta ccccgtgaag tacacacaga ccttcaggct tcacgataac 600
cctgctgtta attacatcta taactgggcc tatggcttcg gatgggcggc caccatcatc 660
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gccgccaagc ccaggtactt ctatccccca gcctaatgtg ggaggaagag cctgagaaaa 780
gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg aacctacgtt 840
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tagtgttaag tttcatgtat gtcgtgtgga gttaaaaaga cttgaattct gtttgctaag 960
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cttgttttaa ctatcagaac actattttgt aaggtgctgc aaagacagtt gaagttttca 1920
ttaccaattt ccccaataaa ccaggtgttc aaatcctgaa aaaaaaaggc 1970

<210> 20
<211> 582
<212> DNA
<213> Mouse

<400> 20
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cacatccaga catcgtcgct ttggtggagg tgtttcgacg agggcggcgg cagcggctcc 180
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cttttctgtg gctttatcat cctgtgcatc tgcttcattc tctcgttctt cgccctgtgt 300
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gataaccctg ctgttaatta catctataac tgggcctatg gcttcggatg ggcggccacc 480
atcatcttga ttggttgttc cttcttcttc tgctgcctcc ccaactacga ggatgacctt 540
ttgggggccg ccaagcccag gtacttctat cccccagcct aa 582

<210> 21
<211> 536
<212> DNA
<213> Rat

<400> 21
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
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ggaggaaagt gttctccaag gagcaaagaa cctatgtttg ggcagtgttc atatgagtgg 480
aaatgctaga ataaatgcta aagaaaattc ttcataaaaa aaaaaaaaaa aaaaaa 536

<210> 22
<211> 375
<212> DNA
<213> Rat

<400> 22
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
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gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaa 375

<210> 23
<211> 471
<212> DNA
<213> Homo sapiens

<400> 23
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tgctccagct gacacgtatc cagctactgg tcctgctgat gatgaagccc ctgatgctga 180
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tggtagagtg tgtccctgag atggaatcag cttgagtctt ctgcaattgg gtcacaacta 360
ttcatgcttc ctgtgatttc atccaactac ttaccttgcc tacgatatcc cctttatctc 420
taatcagttt attttctttc aaataaaaaa taactatgag cgagctaaca t 471

<210> 24
<211> 273
<212> DNA
<213> Homo sapiens

<400> 24
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aatccgacaa cagctgctcc agctgacacg tatccagcta ctggtcctgc tgatgatgaa 120
gcccctgatg ctgaaaccac tgctgctgca accactgcga ccactgctgc tcctaccact 180
gcaaccaccg ctgcttctac cactgctcgt aaagacattc cagttttacc caaatgggtt 240
ggggatctcc cgaatggtag agtgtgtccc tga 273

<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

<400> 25
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
1 5 10 15

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
1 5 10 15

<210> 28
<211> 1555
<212> DNA
<213> Homo sapiens

<400> 28
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tatctcccag cattgttagc tactgagtgg cacatcttca gtacgcatga ttcgtggggg 120
actcaggcag aggtaaaagt gtgaaacttt tcagcattac ctaagaagca aaggctcaat 180
tttggctgct tcattcttat ctcttctgcc acagttctaa cgtgcctgat ctactgagac 240
caaggatgac caatgactca gaagggaaaa tgggatttaa acacccaaag atcatgggga 300
atttcagagg tcatgccctc cctggaacct tctttttttat tattggtctt tggtggtgta 360
caaagagtat tctgaagtat atctgcaaaa agcaaaagcg aacctgctat cttggttcca 420
aaacattatt ctatcgattg gaaattttgg agggaattac aatagttggc atggctttaa 480
ctggcatggc tggggagcag tttattcctg gagggcccca tctgatgtta tatgactata 540
aacaaggtca ctggaatcaa ctcctgggct ggcatcattt caccatgtat ttcttctttg 600
ggctgttggg tgtggcagat atcttatgtt tcaccatcag ttcacttcct gtgtccttaa 660
ccaagttaat gttgtcaaat gccttatttg tggaggcctt tatcttctac aaccacactc 720
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caggcctcgt tgccttccta gagttccttg ttcggaacaa tgtacttctg gagctattgc 840
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aaggttactg ggcttgctac tatttgtaac tccttgacca tggaattata cttgtttatc 1500
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<210> 29
<211> 291
<212> PRT
<213> Homo sapiens

<400> 29

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			20					25					30		
Ile	Gly	Leu	Trp	Trp	Cys	Thr	Lys	Ser	Ile	Leu	Lys	Tyr	Ile	Cys	Lys
		35					40					45			
Lys	Gln	Lys	Arg	Thr	Cys	Tyr	Leu	Gly	Ser	Lys	Thr	Leu	Phe	Tyr	Arg
	50					55					60				
Leu	Glu	Ile	Leu	Glu	Gly	Ile	Thr	Ile	Val	Gly	Met	Ala	Leu	Thr	Gly
65					70					75					80
Met	Ala	Gly	Glu	Gln	Phe	Ile	Pro	Gly	Gly	Pro	His	Leu	Met	Leu	Tyr
				85					90					95	
Asp	Tyr	Lys	Gln	Gly	His	Trp	Asn	Gln	Leu	Leu	Gly	Trp	His	His	Phe
			100					105					110		
Thr	Met	Tyr	Phe	Phe	Phe	Gly	Leu	Leu	Gly	Val	Ala	Asp	Ile	Leu	Cys
		115					120					125			
Phe	Thr	Ile	Ser	Ser	Leu	Pro	Val	Ser	Leu	Thr	Lys	Leu	Met	Leu	Ser
	130					135					140				
Asn	Ala	Leu	Phe	Val	Glu	Ala	Phe	Ile	Phe	Tyr	Asn	His	Thr	His	Gly
145					150					155					160
Arg	Glu	Met	Leu	Asp	Ile	Phe	Val	His	Gln	Leu	Leu	Val	Leu	Val	Val
				165					170					175	
Phe	Leu	Thr	Gly	Leu	Val	Ala	Phe	Leu	Glu	Phe	Leu	Val	Arg	Asn	Asn
			180					185					190		
Val	Leu	Leu	Glu	Leu	Leu	Arg	Ser	Ser	Leu	Ile	Leu	Leu	Gln	Gly	Ser
		195					200					205			
Trp	Phe	Phe	Gln	Ile	Gly	Phe	Val	Leu	Tyr	Pro	Pro	Ser	Gly	Gly	Pro
	210					215					220				
Ala	Trp	Asp	Leu	Met	Asp	His	Glu	Asn	Ile	Leu	Phe	Leu	Thr	Ile	Cys
225					230					235					240
Phe	Cys	Trp	His	Tyr	Ala	Val	Thr	Ile	Val	Ile	Val	Gly	Met	Asn	Tyr
				245					250					255	
Ala	Phe	Ile	Thr	Trp	Leu	Val	Lys	Ser	Arg	Leu	Lys	Arg	Leu	Cys	Ser
			260					265					270		

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
275 280 285

Glu Glu Met
290

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 30
Tyr Pro Pro Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Cys
1 5 10 15

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 31
Cys Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu Glu Glu Met
1 5 10 15

<210> 32
<211> 10320
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (10123)..(10185)
<223> "n" at positions 10123 and 10185 can be any base.

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Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
65 70 75 80

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Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala
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Phe Ser Ser Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro
        115                 120                 125

Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser
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Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
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Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly
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Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp
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Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp
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Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys
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Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile
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Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln
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Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln
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Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser
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Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly
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Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly
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Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
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Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln
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His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
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Lys Leu Glu Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser
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Ser Ser Asp Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu
785                 790                 795                 800

Arg Gly Ser Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro
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Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu
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Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly
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Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys
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Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn
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Ile Arg Arg Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala
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Gly Ser Pro Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His
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Ser Leu Thr Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser Gln
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Thr Lys Ala Pro Pro Asn Val Lys Asn Glu Gly Pro Leu Asn Val Val
1185 1190 1195 1200

Lys Thr Glu Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys
1205 1210 1215

Cys Val His Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu
1220 1225 1230

His Met Ser Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys
1235 1240 1245

Gln His Leu Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg
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Gly Leu His Arg Asn Asn Ala Gln Val Glu Lys Asn Gly Lys Pro Lys
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<210> 34
<211> 5277
<212> DNA
<213> Homo sapiens

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<210> 35
<211> 871
<212> PRT
<213> Homo sapiens

<400> 35

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             20                  25                  30

Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
         35                  40                  45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
     50                  55                  60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
 65                  70                  75                  80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
                 85                  90                  95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
            100                 105                 110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
        115                 120                 125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
    130                 135                 140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145                 150                 155                 160
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Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
                165                 170                 175

Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
            180                 185                 190

Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
        195                 200                 205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
    210                 215                 220

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225                 230                 235                 240

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
                245                 250                 255

Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
            260                 265                 270

Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
        275                 280                 285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
    290                 295                 300

Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305                 310                 315                 320

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
                325                 330                 335

Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
            340                 345                 350

Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
        355                 360                 365

Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
    370                 375                 380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385                 390                 395                 400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
                405                 410                 415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
            420                 425                 430

Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
        435                 440                 445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
    450                 455                 460

Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465                 470                 475                 480
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Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
485 490 495

Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
500 505 510

Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
515 520 525

Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
530 535 540

Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545 550 555 560

Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
565 570 575

His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
580 585 590

Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
595 600 605

Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610 615 620

Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625 630 635 640

Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
645 650 655

Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
660 665 670

Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
675 680 685

Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
690 695 700

Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705 710 715 720

Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
725 730 735

Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
740 745 750

His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
755 760 765

Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
770 775 780

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785 790 795 800

```
Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
                805                 810                 815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
            820                 825                 830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
        835                 840                 845

Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
    850                 855                 860

Leu Trp Asp Gly Trp Glu Gly
865                 870
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<210> 36
<211> 1922
<212> DNA
<213> Homo sapiens

<400> 36

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<210> 37
<211> 1179

<212> DNA
<213> Homo sapiens

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<210> 38
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 38
Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
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Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
20 25 30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
35 40 45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
50 55 60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
65 70 75 80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
85 90 95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
100 105 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
115 120 125

```
Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
    130                 135                 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145                 150                 155                 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165                 170                 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
            180                 185                 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
        195                 200                 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
    210                 215                 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225                 230                 235                 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245                 250                 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
            260                 265                 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275                 280                 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290                 295                 300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305                 310                 315                 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325                 330                 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340                 345                 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390
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<210> 39
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE

<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 39

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Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
  1               5                  10                  15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
             20                  25                  30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
         35                  40                  45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
     50                  55                  60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65                  70                  75                  80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
                 85                  90                  95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
            100                 105                 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
        115                 120                 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
    130                 135                 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145                 150                 155                 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165                 170                 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
            180                 185                 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
        195                 200                 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
    210                 215                 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225                 230                 235                 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245                 250                 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
            260                 265                 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275                 280                 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290                 295                 300
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Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305                 310                 315                 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325                 330                 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340                 345                 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390


<210> 40
<211> 162
<212> PRT
<213> Mouse

<400> 40
Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu Ile Val Val Pro Glu
  1               5                  10                  15

Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu Val Met Arg
             20                  25                  30

Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr
         35                  40                  45

Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile
     50                  55                  60

Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
 65                  70                  75                  80

Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
                85                  90                  95

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
            100                 105                 110

Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln
        115                 120                 125

Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met Phe Pro Arg
    130                 135                 140

Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu Arg Pro
145                 150                 155                 160

Tyr Lys
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<210> 41
<211> 2840
<212> DNA
<213> Homo sapiens

<400> 41
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cgactggagt ttgggggaag aaactctcct gcgccccaga agatttcttc ctcggcgaag 180
ggacagcgaa agatgagggt ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcag 240
cgcgagaggg cagtgccatg ttcctctcca tcctagtggc gctgtgcctg tggctgcacc 300
tggcgctggg cgtgcgcggc gcgccctgcg aggcggtgcg catccctatg tgccggcaca 360
tgccctggaa catcacgcgg atgcccaacc acctgcacca cagcacgcag gagaacgcca 420
tcctggccat cgagcagtac gaggagctgg tggacgtgaa ctgcagcgcc gtgctgcgct 480
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acaaccacag ctggcccgaa agcctggcct gcgacgagct gcctgtctat gaccgtggcg 660
tgtgcatttc gcctgaagcc atcgtcacgg acctcccgga ggatgttaag tggatagaca 720
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cctatctaat cctactctcc actacacaga ggtaatcact attagtattt tggcatatta 2580
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tgtcaagaaa gcagaaacca tctcatttct aacagctgtg ttatattcca tagtatgcat 2760
tactcaacaa actgttgtgc tattggatac ttaggtggtt tcttcactga caatactgaa 2820
taaacatctc accggaattc 2840

<210> 42
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 42
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cggatgccca accacctgca ccacagcacg caggagaacg ccatcctggc catcgagcag 180
tacgaggagc tggtggacgt gaactgcagc gccgtgctgc gcttcttctt ctgtgccatg 240
tacgcgccca tttgcaccct ggagttcctg cacgacccta tcaagccgtg caagtcggtg 300
tgccaacgcg cgcgcgacga ctgcgagccc ctcatgaaga tgtacaacca cagctggccc 360
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gccatcgtca cggacctccc ggaggatgtt aagtggatag acatcacacc agacatgatg 480
gtacaggaaa ggcctcttga tgttgactgt aaacgcctaa gccccgatcg gtgcaagtgt 540
aaaaaggtga agccaacttt ggcaacgtat ctcagcaaaa actacagcta tgttattcat 600
gccaaaataa aagctgtgca gaggagtggc tgcaatgagg tcacaacggt ggtggatgta 660
aaagagatct tcaagtcctc atcacccatc cctcgaactc aagtcccgct cattacaaat 720
tcttcttgcc agtgtccaca catcctgccc catcaagatg ttctcatcat gtgttacgag 780
tggcgttcaa ggatgatgct tcttgaaaat tgcttagttg aaaaatggag agatcagctt 840
agtaaaagat ccatacagtg ggaagagagg ctgcaggaac agcggagaac agttcaggac 900
aagaagaaaa cagccgggcg caccagtcgt agtaatcccc ccaaaccaaa gggaaagcct 960
cctgctccca aaccagccag tcccaagaag aacattaaaa ctaggagtgc ccagaagaga 1020
acaaacccga aaagagtgtg a 1041

<210> 43
<211> 346
<212> PRT
<213> Homo sapiens

<400> 43
Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
1 5 10 15

Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
130 135 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
165 170 175

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Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
            180                 185                 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
        195                 200                 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
    210                 215                 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
225                 230                 235                 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
                245                 250                 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
            260                 265                 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
        275                 280                 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
    290                 295                 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
305                 310                 315                 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
                325                 330                 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
            340                 345
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<210> 44
<211> 749
<212> DNA
<213> Homo sapiens

<400> 44
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cggcaccaag agcactggcc aagtcagctt cttctgagag agtctctaga agacatgatg 60
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gcaataaaaa aggaaaagag gcctcctcag acactctcaa gaggatgggg agatgacatc 180
acttgggtac aaacttatga agaaggtctc ttttatgctc aaaaaagtaa gaagccatta 240
atggttattc atcacctgga ggattgtcaa tactctcaag cactaaagaa agtatttgcc 300
caaaatgaag aaatacaaga aatggctcag aataagttca tcatgctaaa ccttatgcat 360
gaaaccactg ataagaattt atcacctgat gggcaatatg tgcctagaat catgtttgta 420
gacccttctt taacagttag agctgacata gctggaagat actctaacag attgtacaca 480
tatgagcctc gggatttacc cctattgata gaaaacatga agaaagcatt aagacttatt 540
cagtcagagc tataagagat gatagaaaaa agccttcact tcaaagaagt caaatttcat 600
gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgtaata 660
ttactattta gtttttttaa tgtgtttgca atagtcttat taaaataaat gtttttttaaa 720
tctgaaaaaa aaaaaaaaaa aaaaaaaaa                                   749
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<210> 45
<211> 501
<212> DNA
<213> Homo sapiens

<400> 45
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gacatcactt gggtacaaac ttatgaagaa ggtctctttt atgctcaaaa aagtaagaag 180
ccattaatgg ttattcatca cctggaggat tgtcaatact ctcaagcact aaagaaagta 240
tttgcccaaa atgaagaaat acaagaaatg gctcagaata agttcatcat gctaaacctt 300
atgcatgaaa ccactgataa gaatttatca cctgatgggc aatatgtgcc tagaatcatg 360
tttgtagacc cttctttaac agttagagct gacatagctg gaagatactc taacagattg 420
tacacatatg agcctcggga tttaccccta ttgatagaaa acatgaagaa agcattaaga 480
cttattcagt cagagctata a 501

<210> 46
<211> 166
<212> PRT
<213> Homo sapiens

<400> 46
Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr Val
1 5 10 15

Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
20 25 30

Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
35 40 45

Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
50 55 60

Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
65 70 75 80

Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
85 90 95

Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
100 105 110

Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
115 120 125

Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
130 135 140

Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
145 150 155 160

Leu Ile Gln Ser Glu Leu
165

<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 47
agcggccggg gccacgatgg agcgcgacgg ctgcgcgggg ggcgggagcc gcggcggcga 60

gggcgggcgc gctccccggg agggcccggc ggggaacggc cgcgatcggg gccgcagcca 120
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gggggaggag ccgctggaga aggcggcgcg cgcccgcact gccaaggacc ccaacaccta 240
taaagtactc tcgctggtat tgtcagtatg tgtgttaaca acaatacttg gttgtatatt 300
tgggttgaaa ccaagctgtg ccaaagaagt taaaagttgc aaaggtcgct gtttcgagag 360
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ttaccaggag acgtgcatag aaccagaaca tatatggact tgcaacaaat tcaggtgtgg 480
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tagcaaacta aaaaaatgtg gaacatatac taaaaacatg agaccggtat atccaacaaa 780
aactttcccc aatcactaca gcattgtcac cggattgtat ccagaatctc atggcataat 840
cgacaataaa atgtatgatc ccaaaatgaa tgcttccttt tcacttaaaa gtaaagagaa 900
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aatgagttca actttgaggg acgatctttg aatatactta cctattataa aatcttactt 3480
tgtatttgta ttt 3493

<210> 48
<211> 925
<212> PRT
<213> Homo sapiens

<400> 48
Met Glu Arg Asp Gly Cys Ala Gly Gly Gly Ser Arg Gly Gly Glu Gly
1 5 10 15

Gly Arg Ala Pro Arg Glu Gly Pro Ala Gly Asn Gly Arg Asp Arg Gly
20 25 30

Arg Ser His Ala Ala Glu Ala Pro Gly Asp Pro Gln Ala Ala Ala Ser
35 40 45

Leu Leu Ala Pro Met Asp Val Gly Glu Glu Pro Leu Glu Lys Ala Ala
50 55 60

Arg Ala Arg Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu
65 70 75 80

Val Leu Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly
85 90 95

Leu Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
100 105 110

Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val Glu
115 120 125

Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu Pro Glu
130 135 140

His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys Arg Leu Thr
145 150 155 160

Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp Lys Gly Asp Cys
165 170 175

Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu Lys Ser Trp Val Glu
180 185 190

Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln Cys Pro Ala Gly Phe Glu
195 200 205

Thr Pro Pro Thr Leu Leu Phe Ser Leu Asp Gly Phe Arg Ala Glu Tyr
210 215 220

Leu His Thr Trp Gly Gly Leu Leu Pro Val Ile Ser Lys Leu Lys Lys
225 230 235 240

Cys Gly Thr Tyr Thr Lys Asn Met Arg Pro Val Tyr Pro Thr Lys Thr
245 250 255

Phe Pro Asn His Tyr Ser Ile Val Thr Gly Leu Tyr Pro Glu Ser His
260 265 270

Gly Ile Ile Asp Asn Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe
275 280 285

Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
290 295 300

Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
305 310 315 320

Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
325 330 335

Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
340 345 350

Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr
355 360 365

Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
370 375 380

Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
385 390 395 400

Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
405 410 415

Asn Leu Ile Leu Ile Ser Asp His Gly Met Glu Gln Gly Ser Cys Lys
420 425 430

Lys Tyr Ile Tyr Leu Asn Lys Tyr Leu Gly Asp Val Lys Asn Ile Lys
435 440 445

Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
450 455 460

Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
465 470 475 480

Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
485 490 495

Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
500 505 510

Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
515 520 525

Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
530 535 540

Gln Ala Leu Phe Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu
545 550 555 560

Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
565 570 575

Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
580 585 590

His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
595 600 605

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His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
    610                 615                 620

Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr
625                 630                 635                 640

Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
                645                 650                 655

Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
            660                 665                 670

Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
        675                 680                 685

Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
    690                 695                 700

Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
705                 710                 715                 720

Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
                725                 730                 735

Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
            740                 745                 750

Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
        755                 760                 765

Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
    770                 775                 780

Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
785                 790                 795                 800

Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
                805                 810                 815

Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
            820                 825                 830

Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
        835                 840                 845

Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
    850                 855                 860

Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
865                 870                 875                 880

Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
                885                 890                 895

Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu
            900                 905                 910

Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
        915                 920                 925
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<210> 49
<211> 2709
<212> DNA
<213> Homo sapiens

<400> 49
ggttttcaaa tggaacattt tgatgcatca cttagtacct atttcaaggc attgctaggc 60
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tgctctgtca tatatttact aattgtatgg ctgggaccaa aatacatgag gaataaacag 180
ccattctctt gccgggggat tttagtggtg tataaccttg gactcacact gctgtctctg 240
tatatgttct gtgagttagt aacaggagta tgggaaggca aatacaactt cttctgtcag 300
ggcacacgca ccgcaggaga atcagatatg aagattatcc gtgtcctctg gtggtactac 360
ttctccaaac tcatagaatt tatggacact ttcttcttca tcctgcgcaa gaacaaccac 420
cagatcacgg tcctgcacgt ctaccaccat gcctcgatgc tgaacatctg gtggtttgtg 480
atgaactggg tcccctgcgg ccactcttat tttggtgcca cacttaatag cttcatccac 540
gtcctcatgt actcttacta tggtttgtcg tcagtccctt ccatgcgtcc atacctctgg 600
tggaagaagt acatcactca ggggcagctg cttcagtttg tgctgacaat catccagacc 660
agctgcgggg tcatctggcc gtgcacattc cctcttggtt ggttgtattt ccagattgga 720
tacatgattt ccctgattgc tctcttcaca aacttctaca ttcagaccta caacaagaaa 780
ggggcctccc gaaggaaaga ccacctgaag gaccaccaga atgggtccat ggctgctgtg 840
aatggacaca ccaacagctt ttcacccctg gaaaacaatg tgaagccaag gaagctgcgg 900
aaggattgaa gtcaaagaat tgaaaccctc caaaccacgt catctgattg taagcacaat 960
atgagttgtg ccccaatgct cgttaacagc tgctgtaact agtctggcct acaatagtgt 1020
gattcatgta ggacttcttt catcaattca aaacccctag aaaacgtata cagattatat 1080
aagtagggat aagatttcta acatttctgg gctctctgac ccctgcgcta gactgtggaa 1140
agggagtatt attatagtat acaacactgc tgttgcctta ttagttataa catgataggt 1200
gctgaattgt gattcacaat ttaaaaacac tgtaatccaa acttttttt ttaactgtag 1260
atcatgcatg tgattgtaaa tgtaaatttg tacaatgttg ttatggtaga gaaacacaca 1320
tgccttaaaa tttaaaaagc agggcccaaa gcttattagt ttaaattagg gtatgtttca 1380
agtttgtatt aatttgtaat agctctgttt agaaaaaatc aaagaccatg atttatgaaa 1440
ctaatgtgac ataatttcca gtgacttgtt gatgtgaaat cagacacggc accttcagtt 1500
ttgtactatt ggctttgaat caagcaggct caaatctagt ggaacagtca gtttaacttt 1560
ttaacagatc ttatttttt attttgagtg ccactattaa tgtaaaaagg gggggctct 1620
acagcagtcg tgatgaaact taaatatata ttctttgtcc tcgagatttt aggaagggtg 1680
tagggtgagt aggccatttt taatttctga agtgctaagt gtttttatac agcaaacaaa 1740
aagtcaattt tgctttccac cagtgcgaga gaggatgtat acttttcaag agagatgatt 1800
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gcctagttta ccaaaattaa caaaggggg gaaaggacct tagaactttt taaggtaaaa 1980
tcaaatatag ctacagcata agagaatcga gaaatttgat agaggtaact tgtttaatgt 2040
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ttgtttaaaa ataatagact gcttatcata aaatcacatc tcacacattt gaggcagtgg 2160
tcaaacaggt aaagcctatg atgtgtgtca ttttaaagtg tcggaattta gcctctgaat 2220
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ttgacaatgt ataaactaat tgttggtttg atatttatgt aaatatcagt ttaccatgct 2340
ttaattttgc acattcgtac tatagggagc ctattggttc tctattagtc ttgtgggttt 2400
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atatttataa atgtatgtct tcattgctag gtactaattt gcagatgtct ttacatattt 2520
caatacagaa actataacat tcaatagtgt gctgtcaaag tgtgcttagc tcacctggat 2580
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aaaaaaaaa 2709

<210> 50
<211> 299
<212> PRT
<213> Homo sapiens

<400> 50

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Gly Pro Arg Asp Thr Arg Val Lys Gly Trp Phe Leu Leu Asp Asn Tyr
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Ile Pro Thr Phe Ile Cys Ser Val Ile Tyr Leu Leu Ile Val Trp Leu
         35                  40                  45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
     50                  55                  60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
 65                  70                  75                  80

Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
                 85                  90                  95

Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
            100                 105                 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
        115                 120                 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Val Leu His Val
    130                 135                 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
145                 150                 155                 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
                165                 170                 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
            180                 185                 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
        195                 200                 205

Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
    210                 215                 220

Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
225                 230                 235                 240

Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
                245                 250                 255

Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
            260                 265                 270

Ser Met Ala Ala Val Asn Gly His Thr Asn Ser Phe Ser Pro Leu Glu
        275                 280                 285

Asn Asn Val Lys Pro Arg Lys Leu Arg Lys Asp
    290                 295
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<210> 51

<211> 1019
<212> DNA
<213> Homo sapiens

<400> 51
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ccagggaagg acctttcacc ttgactatat ggcattatgt catcacaagc tctgaggctt 120
ctcctttcca tcctgcgtgg acagctaaga cctcagtttt caatagcatc tagagcagtg 180
ggactcagct ggggtgattt cgccccccat ctccggggga atgtctgaag acaattttgg 240
ttacctcaat gagggagtgg aggaggatac agtgctacta ccaactagtg gataaaggcc 300
agggatgctg ctcaacctcc taccatgtac aggacgtctc cccattacaa ctacccaatc 360
cgaagtgtca actgtgtcag gactaagaaa ccctggtttt gagtagaaaa gggcctggaa 420
agaggggagc caacaaatct gtctgcttcc tcacattagt cattggcaaa taagcattct 480
gtctctttgg ctgctgcctc agcacagaga gccagaactc tatcgggcac caggataaca 540
tctctcagtg aacagagttg acaaggccta tgggaaatgc ctgatgggat tatcttcagc 600
ttgttgagct tctaagtttc tttcccttca ttctaccctg caagccaagt tctgtaagag 660
aaatgcctga gttctagctc aggttttctt actctgaatt tagatctcca gacccttcct 720
ggccacaatt caaattaagg caacaaacat ataccttcca tgaagcacac acagactttt 780
gaaagcaagg acaatgactg cttgaattga ggccttgagg aatgaagctt tgaaggaaaa 840
gaatactttg tttccagccc ccttcccaca ctcttcatgt gttaaccact gccttcctgg 900
accttggagc cacggtgact gtattacatg ttgttataga aaactgattt tagagttctg 960
atcgttcaag agaatgatta aatatacatt tcctacamaa aaaaaaaaaa aagtcgacg 1019

<210> 52
<211> 1332
<212> DNA
<213> Homo sapiens

<400> 52
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ctttggcctc ggcctcccaa agtgcatgag ccaccatgcc tggcctgttt agttttgttt 120
caagttgaaa taccttttctt gtgttttcta attagaaaag taatatctac tcattgtaaa 180
aactcaaaca gtgcagaaat gtagaaagta gaaagtgtaa gtccctggtt gtcccttctg 240
cctgagcaca accactgctc acagtttgat gtatatcctt ccagagactc tcaaatttaa 300
gcaaataatt tttattacca tgtcttttta tttgaagacg tacatttgcc tccaaagttc 360
aacacaagtt caactgacca tatccttcca tgacctgaat agatgctatc ctttatcacg 420
atgttcaatt gcctttgaaa gagagtagtc caggtatatt cctgatcaaa atttggcatt 480
tttgatgata ctactctaca cagatcagac tcatgtgcag aatcgtgcct ggagagagag 540
gtttggttaa gacagagatt tctggaaaca ttcaaattgc aaatggaaac ttgaaaccca 600
caatctaatg aggaatgtac tggaaaaata atctgaagag ttgacaaatt gtgtactaga 660
ttgaacacat ggaatgcaat gccaatgaga ctttctgcac taaaacttat cctcatatgt 720
acaacaatga tgtgtgtatt atataacagt gatgtgtaca tttctgacac cccatacata 780
atatacacag tttgtataaa tgcatacatt taaaaatata tatgtacaat acagctaaca 840
taaaactgta gtacgcctga aggatattac tagtgcctaa tattgagtat gagtcactgc 900
gtgttcgcat caacttggaa gtgcagtaat tgttataaaa ttaatcagtg cagccaacat 960
tatttatgaa tcacatcttt gaaactgtgc agtagcatat acatatatat ttttaaataa 1020
cattttcac agttttccag agttactgtt gaaatctgca tcaccaaaaa aaaaaaaaag 1080
caagattttt ttaacaatgt agacactctt cagacccagt aatctgcgtg tgatttccta 1140
tttgtagatt cccaagagac tttagcagtc accagcctta atgcatgtac aggatattat 1200
tgtgacttaa tttatctgca gtttttaatc catgtgaaat tgggaatttt taaccgaact 1260
tggattaacc atgcctgcct ttctaaggtt gcaaatgtta cattaaatga tttatgttgt 1320
aaaaaaaaaa aa 1332

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (3)
<223> "Xaa" at position 3 can be any amino acid

<220>
<223> Description of Artificial Sequence: Ctyokine
receptor exctracellular motif found in many
species.

<400> 53
Trp Ser Xaa Trp Ser
1 5

<210> 54
<211> 2744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(2387)

<400> 54
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ccagtgggcc cgtgtggaac caaacctgcg cgcgtggccg ggccgtggga caacgaggcc 120

gcggagacga aggcgca atg gcg agg aag tta tct gta atc ttg atc ctg 170
Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu
1 5 10

acc ttt gcc ctc tct gtc aca aat ccc ctt cat gaa cta aaa gca gct 218
Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala
15 20 25

gct ttc ccc cag acc act gag aaa att agt ccg aat tgg gaa tct ggc 266
Ala Phe Pro Gln Thr Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly
30 35 40

att aat gtt gac ttg gca att tcc aca cgg caa tat cat cta caa cag 314
Ile Asn Val Asp Leu Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln
45 50 55

ctt ttc tac cgc tat gga gaa aat aat tct ttg tca gtt gaa ggg ttc 362
Leu Phe Tyr Arg Tyr Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe
60 65 70 75

aga aaa tta ctt caa aat ata ggc ata gat aag att aaa aga atc cat 410
Arg Lys Leu Leu Gln Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His
80 85 90

ata cac cat gac cac gac cat cac tca gac cac gag cat cac tca gac 458
Ile His His Asp His Asp His His Ser Asp His Glu His His Ser Asp
95 100 105

cat gag cgt cac tca gac cat gag cat cac tca gac cac gag cat cac 506
His Glu Arg His Ser Asp His Glu His His Ser Asp His Glu His His
110 115 120

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tct gac cat aat cat gct gct tct ggt aaa aat aag cga aaa gct ctt   554
Ser Asp His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu
    125                 130                 135

tgc cca gac cat gac tca gat agt tca ggt aaa gat cct aga aac agc   602
Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser
140                 145                 150                 155

cag ggg aaa gga gct cac cga cca gaa cat gcc agt ggt aga agg aat   650
Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg Asn
                160                 165                 170

gtc aag gac agt gtt agt gct agt gaa gtg acc tca act gtg tac aac   698
Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn
            175                 180                 185

act gtc tct gaa gga act cac ttt cta gag aca ata gag act cca aga   746
Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg
        190                 195                 200

cct gga aaa ctc ttc ccc aaa gat gta agc agc tcc act cca ccc agt   794
Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser
    205                 210                 215

gtc aca tca aag agc cgg gtg agc cgg ctg gct ggt agg aaa aca aat   842
Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn
220                 225                 230                 235

gaa tct gtg agt gag ccc cga aaa ggc ttt atg tat tcc aga aac aca   890
Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr
                240                 245                 250

aat gaa aat cct cag gag tgt ttc aat gca tca aag cta ctg aca tct   938
Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser
            255                 260                 265

cat ggc atg ggc atc cag gtt ccg ctg aat gca aca gag ttc aac tat   986
His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr
        270                 275                 280

ctc tgt cca gcc atc atc aac caa att gat gct aga tct tgt ctg att  1034
Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile
    285                 290                 295

cat aca agt gaa aag aag gct gaa atc cct cca aag acc tat tca tta  1082
His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu
300                 305                 310                 315

caa ata gcc tgg gtt ggt ggt ttt ata gcc att tcc atc atc agt ttc  1130
Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe
                320                 325                 330

ctg tct ctg ctg ggg gtt atc tta gtg cct ctc atg aat cgg gtg ttt  1178
Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val Phe
            335                 340                 345

ttc aaa ttt ctc ctg agt ttc ctt gtg gca ctg gcc gtt ggg act ttg  1226
Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu
        350                 355                 360
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agt ggt gat gct ttt tta cac ctt ctt cca cat tct cat gca agt cac   1274
Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser His
    365                 370                 375

cac cat agt cat agc cat gaa gaa cca gca atg gaa atg aaa aga gga   1322
His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg Gly
380                 385                 390                 395

cca ctt ttc agt cat ctg tct tct caa aac ata gaa gaa agt gcc tat   1370
Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr
                400                 405                 410

ttt gat tcc acg tgg aag ggt cta aca gct cta gga ggc ctg tat ttc   1418
Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe
            415                 420                 425

atg ttt ctt gtt gaa cat gtc ctc aca ttg atc aaa caa ttt aaa gat   1466
Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp
        430                 435                 440

aag aag aaa aag aat cag aag aaa cct gaa aat gat gat gat gtg gag   1514
Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu
    445                 450                 455

att aag aag cag ttg tcc aag tat gaa tct caa ctt tca aca aat gag   1562
Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu
460                 465                 470                 475

gag aaa gta gat aca gat gat cga act gaa ggc tat tta cga gca gac   1610
Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp
                480                 485                 490

tca caa gag ccc tcc cac ttt gat tct cag cag cct gca gtc ttg gaa   1658
Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu
            495                 500                 505

gaa gaa gag gtc atg ata gct cat gct cat cca cag gaa gtc tac aat   1706
Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr Asn
        510                 515                 520

gaa tat gta ccc aga ggg tgc aag aat aaa tgc cat tca cat ttc cac   1754
Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe His
    525                 530                 535

gat aca ctc ggc cag tca gac gat ctc att cac cac cat cat gac tac   1802
Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp Tyr
540                 545                 550                 555

cat cat att ctc cat cat cac cac cac caa aac cac cat cct cac agt   1850
His His Ile Leu His His His His His Gln Asn His His Pro His Ser
                560                 565                 570

cac agc cag cgc tac tct cgg gag gag ctg aaa gat gcc ggc gtc gcc   1898
His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala
            575                 580                 585

act ttg gcc tgg atg gtg ata atg ggt gat ggc ctg cac aat ttc agc   1946
Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe Ser
        590                 595                 600
```

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gat ggc cta gca att ggt gct gct ttt act gaa ggc tta tca agt ggt   1994
Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly
    605                 610                 615

tta agt act tct gtt gct gtg ttc tgt cat gag ttg cct cat gaa tta   2042
Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu Leu
620                 625                 630                 635

ggt gac ttt gct gtt cta cta aag gct ggc atg acc gtt aag cag gct   2090
Gly Asp Phe Ala Val Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala
                640                 645                 650

gtc ctt tat aat gca ttg tca gcc atg ctg gcg tat ctt gga atg gca   2138
Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala
            655                 660                 665

aca gga att ttc att ggt cat tat gct gaa aat gtt tct atg tgg ata   2186
Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile
        670                 675                 680

ttt gca ctt act gct ggc tta ttc atg tat gtt gct ctg gtt gat atg   2234
Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met
    685                 690                 695

gta cct gaa atg ctg cac aat gat gct agt gac cat gga tgt agc cgc   2282
Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser Arg
700                 705                 710                 715

tgg ggg tat ttc ttt tta cag aat gct ggg atg ctt ttg ggt ttt gga   2330
Trp Gly Tyr Phe Phe Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly
                720                 725                 730

att atg tta ctt att tcc ata ttt gaa cat aaa atc gtg ttt cgt ata   2378
Ile Met Leu Leu Ile Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile
            735                 740                 745

aat ttc tag ttaaggttta aatgctagag tagcttaaaa agttgtcata           2427
Asn Phe

gtttcagtag gtcataggga gatgagtttg tatgctgtac tatgcagcgt ttaaagttag 2487

tgggttttgt gatttttgta ttgaatattg ctgtctgtta caaagtcagt taaaggtacg 2547

ttttaatatt taagttattc tatcttggag ataaaatctg tatgtgcaat tcaccggtat 2607

taccagttta ttatgtaaac aagagatttg gcatgacatg ttctgtatgt ttcagggaaa 2667

aatgtcttta atgctttttc aagaactaac acagttattc ctatactgga ttttaggtct 2727

ctgaagaact gctggtg                                               2744
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<210> 55
<211> 000
<212> 000
<213> 000

<400> 55

000

<210> 56
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (190)
<223> "n" at position 190 can be any base

<400> 56
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acgaccacca acatgaatca gtttgtaggc atttacaagc cacagctgaa aataaaaatc 120
tgtctgtgtt gaataggcat ttaacaaatt acttgaaaac tgcaagaatc ataattatta 180
taaatttaan gtttgtgatt caaacatggg taagatcaca gtcatgggga gaagcccaac 240
agattcctgt gatgatcctt attttcttcc tatatcttta tatacatagg agg 293

<210> 57
<211> 2053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)..(1347)

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Ala Leu Asn Leu Ser Gly Ser Arg Leu Asp Glu Val Arg Ala Gly Ala
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Phe Glu His Leu Pro Ser Leu Arg Gln Leu Asp Leu Ser His Asn Pro
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ctg gcc gac ctc agt ccc ttc gct ttc tcg ggc agc aat gcc agc gtc   591
Leu Ala Asp Leu Ser Pro Phe Ala Phe Ser Gly Ser Asn Ala Ser Val
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tcg gcc ccc agt ccc ctt gtg gaa ctg atc ctg aac cac atc gtg ccc   639
Ser Ala Pro Ser Pro Leu Val Glu Leu Ile Leu Asn His Ile Val Pro
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cct gaa gat gag cgg cag aac cgg agc ttc gag ggc atg gtg gtg gcg   687
Pro Glu Asp Glu Arg Gln Asn Arg Ser Phe Glu Gly Met Val Val Ala
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gcc ctg ctg gcg ggc cgt gca ctg cag ggg ctc cgc cgc ttg gag ctg   735
Ala Leu Leu Ala Gly Arg Ala Leu Gln Gly Leu Arg Arg Leu Glu Leu
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gcc agc aac cac ttc ctt tac ctg ccg cgg gat gtg ctg gcc caa ctg   783
Ala Ser Asn His Phe Leu Tyr Leu Pro Arg Asp Val Leu Ala Gln Leu
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Pro Ser Leu Arg His Leu Asp Leu Ser Asn Asn Ser Leu Val Ser Leu
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acc tac gtg tcc ttc cgc aac ctg aca cat cta gaa agc ctc cac ctg   879
Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser Leu His Leu
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gag gac aat gcc ctc aag gtc ctt cac aat ggc acc ctg gct gag ttg   927
Glu Asp Asn Ala Leu Lys Val Leu His Asn Gly Thr Leu Ala Glu Leu
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Gln Gly Leu Pro His Ile Arg Val Phe Leu Asp Asn Asn Pro Trp Val
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Cys Asp Cys His Met Ala Asp Met Val Thr Trp Leu Lys Glu Thr Glu
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Val Val Gln Gly Lys Asp Arg Leu Thr Cys Ala Tyr Pro Glu Lys Met
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Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn
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cgc aag ggg ata aaa aag tgg atg cat aac atc aga gat gcc tgc agg   1263
Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg
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gat cac atg gaa ggg tat cat tac aga tat gaa atc aat gcg gac ccc   1311
Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro
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aga tta aca aac ctc agt tct aac tcg gat gtc tga gaaatattag        1357
Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
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Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu
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Phe Ile Phe Leu Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys
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Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe
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Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val
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Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys
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gat ata gct tca tta aat att cag ctc act tgc aac att ctt aca ttc   579
Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe
         95                 100                 105

gga cag ctt gaa cag aat gtt tat gga atc aca ata att tca ggc ttg   627
Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu
    110                 115                 120

cct cca gaa aaa cct aaa aat ttg agt tgc att gtg aac gag ggg aag   675
Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys
125                 130                 135                 140

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Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr
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aac ttc act tta aaa tct gaa tgg gca aca cac aag ttt gct gat tgc   771
Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys
            160                 165                 170

aaa gca aaa cgt gac acc ccc acc tca tgc act gtt gat tat tct act   819
Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr
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gtg tat ttt gtc aac att gaa gtc tgg gta gaa gca gag aat gcc ctt   867
Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu
    190                 195                 200

ggg aag gtt aca tca gat cat atc aat ttt gat cct gta tat aaa gtg   915
Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val
205                 210                 215                 220

aag ccc aat ccg cca cat aat tta tca gtg atc aac tca gag gaa ctg   963
Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu
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tct agt atc tta aaa ttg aca tgg acc aac cca agt att aag agt gtt   1011
Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val
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Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr
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Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe
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Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg
285                 290                 295                 300

tgt atg aag gaa gat ggt aag gga tac tgg agt gac tgg agt gaa gaa   1203
Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu
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Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln
        335                 340                 345

ctc gtg tgg aag aca ttg cct cct ttt gaa gcc aat gga aaa atc ttg   1347
Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu
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gat tat gaa gtg act ctc aca aga tgg aaa tca cat tta caa aat tac   1395
Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr
365                 370                 375                 380

aca gtt aat gcc aca aaa ctg aca gta aat ctc aca aat gat cgc tat   1443
Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr
                385                 390                 395

cta gca acc cta aca gta aga aat ctt gtt ggc aaa tca gat gca gct   1491
Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala
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Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met
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gat ctt aaa gca ttc ccc aaa gat aac atg ctt tgg gtg gaa tgg act   1587
Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr
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act cca agg gaa tct gta aag aaa tat ata ctt gag tgg tgt gtg tta   1635
Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu
445                 450                 455                 460

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Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr
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gtg cat cgc acc tat tta aga ggg aac tta gca gag agc aaa tgc tat   1731
Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr
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ttg ata aca gtt act cca gta tat gct gat gga cca gga agc cct gaa   1779
Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu
        495                 500                 505

tcc ata aag gca tac ctt aaa caa gct cca cct tcc aaa gga cct act   1827
Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr
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gtt cgg aca aaa aaa gta ggg aaa aac gaa gct gtc tta gag tgg gac   1875
Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp
525                 530                 535                 540

caa ctt cct gtt gat gtt cag aat gga ttt atc aga aat tat act ata   1923
Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile
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Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr
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Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro
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gaa ttc act ttt act acc cca aag ttt gct caa gga gaa att gaa gcc   2115
Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala
605                 610                 615                 620

ata gtc gtg cct gtt tgc tta gca ttc cta ttg aca act ctt ctg gga   2163
Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly
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gtg ctg ttc tgc ttt aat aag cga gac cta att aaa aaa cac atc tgg   2211
Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp
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cct aat gtt cca gat cct tca aag agt cat att gcc cag tgg tca cct   2259
Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro
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cac act cct cca agg cac aat ttt aat tca aaa gat caa atg tat tca   2307
His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser
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gat ggc aat ttc act gat gta agt gtt gtg gaa ata gaa gca aat gac   2355
Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp
685                 690                 695                 700

aaa aag cct ttt cca gaa gat ctg aaa tca ttg gac ctg ttc aaa aag   2403
Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys
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gaa aaa att aat act gaa gga cac agc agt ggt att ggg ggg tct tca   2451
Glu Lys Ile Asn Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser
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tgc atg tca tct tct agg cca agc att tct agc agt gat gaa aat gaa   2499
Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu
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Ser Ser Gln Asn Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His
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Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser
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Gln Tyr Phe Lys Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile
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tca cat ttt gaa agg tca aag caa gtt tca tca gtc aat gag gaa gat   2787
Ser His Phe Glu Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp
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Phe Val Arg Leu Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys
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Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala
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